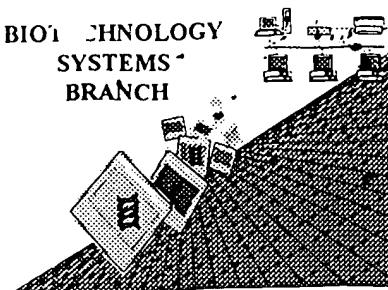


## RAW SEQUENCE LISTING ERROR REPORT

BIOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931007

Source: O I P E

Date Processed by STIC: 08/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/931007

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos:      was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
     prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering                      use space characters, instead.
  
- 4      Non-ASCII              The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
     each n or Xaa can only represent a single residue. Please present the maximum number of each  
     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0          A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)         . Normally, PatentIn would automatically generate this section from the  
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
     Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)              (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)              <210> sequence id number  
                                     <400> sequence id number  
                                     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)              Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>          Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                                     is Artificial Sequence
  
- 11    ✓ Use of <220>          Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                                     "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0          Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,007

DATE: 08/27/2001

TIME: 12:54:35

Input Set : A:\ES.txt

Output Set: N:\CRF3\08272001\I931007.raw

3 <110> APPLICANT: Aventis Pharma S.A.  
 5 <120> TITLE OF INVENTION: SYSTEM FOR REGULATING IN VIVO THE EXPRESSION OF A TRANSGENE  
 BY  
 6       CONDITIONAL INHIBITION  
 8 <130> FILE REFERENCE: 03806.0512  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/931,007  
 C--> 10 <141> CURRENT FILING DATE: 2001-08-17  
 10 <150> PRIOR APPLICATION NUMBER: FR 00/10730  
 11 <151> PRIOR FILING DATE: 2000-08-18  
 13 <150> PRIOR APPLICATION NUMBER: US 60/239,246  
 14 <151> PRIOR FILING DATE: 2000-10-11  
 16 <160> NUMBER OF SEQ ID NOS: 11  
 18 <170> SOFTWARE: PatentIn version 3.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 688  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Homo sapiens,  
 25 <220> FEATURE:  
 W--> 26 <221> NAME/KEY: misc *OK*  
 27 <222> LOCATION: (1)..(688)  
 28 <223> OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-  
 gamma (P  
 29       erxisome Proliferator Activated Receptor-gamma)  
 32 <400> SEQUENCE: 1  
 34 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
 35 1                               5                               10                               15  
 37 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val  
 38                               20                               25                               30  
 40 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val  
 41                               35                               40                               45  
 43 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
 44                               50                               55                               60  
 46 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
 47 65                               70                               75                               80  
 49 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
 50                               85                               90                               95  
 52 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
 53                               100                               105                               110  
 55 Pro Pro Tyr Thr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Asn Lys Cys  
 56                               115                               120                               125  
 58 Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn  
 59                               130                               135                               140  
 61 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu  
 62 145                               150                               155                               160  
 64 Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp  
 65                               165                               170                               175  
 67 Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe  
 68                               180                               185                               190

Does Not Comply  
 Corrected Diskette Needed  
*See page 4 of 7*

70 Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr

## RAW SEQUENCE LISTING

DATE: 08/27/2001

PATENT APPLICATION: US/09/931,007

TIME: 12:54:35

Input Set : A:\ES.txt

Output Set: N:\CRF3\08272001\I931007.raw

```

71          195          200          205
73 Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
74          210          215          220
76 Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
77 225          230          235          240
79 Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val
80          245          250          255
82 Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe
83          260          265          270
85 Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
86          275          280          285
88 His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
89          290          295          300
91 Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
92 305          310          315          320
94 Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
95          325          330          335
97 Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
98          340          345          350
100 Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
101          355          360          365
103 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
104          370          375          380
106 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
107 385          390          395          400
109 Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
110          405          410          415
112 Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
113          420          425          430
115 Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu
116          435          440          445
118 Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
119          450          455          460
121 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro
122 465          470          475          480
124 Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys
125          485          490          495
127 Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys
128          500          505          510
130 Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu
131          515          520          525
133 Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu
134          530          535          540
136 Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr
137 545          550          555          560
139 Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu
140          565          570          575
142 Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp
143          580          585          590

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,007

DATE: 08/27/2001

TIME: 12:54:35

Input Set : A:\ES.txt

Output Set: N:\CRF3\08272001\I931007.raw

```

145 Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg
146      595                        600                        605
148 Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu
149      610                        615                        620
151 Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser
152 625                        630                        635                        640
154 Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile
155                        645                        650                        655
157 Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr
158                        660                        665                        670
160 Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
161      675                        680                        685
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 19
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
W--> 168 <220> FEATURE: Errored
W--> 168 <223> OTHER INFORMATION: A 213 response of "Artificial Sequence" requires
168 <400> SEQUENCE: 2 an explanation or description of the genetic source
169 tcaaccttta ccctggtag in field 223 19
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 13
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
W--> 177 <220> FEATURE:
W--> 177 <223> OTHER INFORMATION:
177 <400> SEQUENCE: 3
178 aggtcaaagg tca
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 30
183 <212> TYPE: DNA
C--> 184 <213> ORGANISM: Artificial primer
W--> 186 <220> FEATURE:
W--> 186 <223> OTHER INFORMATION:
186 <400> SEQUENCE: 4
187 atgcatcgat ggccgcttcg agcagacatg 30
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 39
192 <212> TYPE: DNA
C--> 193 <213> ORGANISM: Artificial primer
W--> 195 <220> FEATURE:
W--> 195 <223> OTHER INFORMATION:
195 <400> SEQUENCE: 5
196 atgcgtcgac tctagccgat tttaccacat ttgtagagg 39
199 <210> SEQ ID NO: 6
200 <211> LENGTH: 33
201 <212> TYPE: DNA
C--> 202 <213> ORGANISM: Artificial primer
W--> 204 <220> FEATURE:

```

*The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,007

DATE: 08/27/2001

TIME: 12:54:35

Input Set : A:\ES.txt

Output Set: N:\CRF3\08272001\I931007.raw

```

W--> 204 <223> OTHER INFORMATION:
      204 <400> SEQUENCE: 6
      205 cgagcatgct gctgctgctg ctgctgctgg gcc
      208 <210> SEQ ID NO: 7
      209 <211> LENGTH: 33
      210 <212> TYPE: DNA
C--> 211 <213> ORGANISM: Artificial primer
W--> 213 <220> FEATURE:
W--> 213 <223> OTHER INFORMATION:
      213 <400> SEQUENCE: 7
      214 ggggtctagat taacccgggt ggcgggcgtc ggt
      217 <210> SEQ ID NO: 8
      218 <211> LENGTH: 20
      219 <212> TYPE: DNA
C--> 220 <213> ORGANISM: Artificial primer
W--> 222 <220> FEATURE:
W--> 222 <223> OTHER INFORMATION:
      222 <400> SEQUENCE: 8
      223 cgatcatgtt cgacgacgcc
      226 <210> SEQ ID NO: 9
      227 <211> LENGTH: 20
      228 <212> TYPE: DNA
C--> 229 <213> ORGANISM: Artificial primer
W--> 231 <220> FEATURE:
W--> 231 <223> OTHER INFORMATION:
      231 <400> SEQUENCE: 9
      232 ccaggtcgca ggcgggtgtag
      235 <210> SEQ ID NO: 10
      236 <211> LENGTH: 23
      237 <212> TYPE: RNA
      238 <213> ORGANISM: Artificial sequence, aptamer
W--> 240 <220> FEATURE:
W--> 240 <223> OTHER INFORMATION:
      240 <400> SEQUENCE: 10
      241 ggccugggcg agaaguuuag gcc
      244 <210> SEQ ID NO: 11
      245 <211> LENGTH: 72
      246 <212> TYPE: RNA
      247 <213> ORGANISM: Artificial sequence, aptamer
W--> 249 <220> FEATURE:
W--> 249 <223> OTHER INFORMATION:
      249 <400> SEQUENCE: 11
      250 ggugaucaga uucugaucca auguuaugcu ucucugccug ggaacagcug ccugaagcuu
      252 uggauccguc gc

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/931,007

DATE: 08/27/2001

TIME: 12:54:36

Input Set : A:\ES.txt

Output Set: N:\CRF3\08272001\I931007.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:168 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:168 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:177 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:177 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:186 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:186 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:193 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:195 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:195 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:202 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:204 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:204 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:211 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:213 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:213 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:220 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:222 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:222 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:229 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:231 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:240 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:240 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:249 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:249 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: